RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	
Source:	TFWP
Date Processed by STIC:	01/11/2007

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/561,292

DATE: 01/11/2007 TIME: 09:48:35

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\01112007\J561292.raw

```
4 <110 > APPLICANT: BOUGUELERET; Lydie
  5 CUSIN; Isabelle
  7 <120> TITLE OF INVENTION: SECRETED POLYPEPTIDE SPECIES ASSOCIATED
        WITH CARDIOVASCULAR DISORDERS
 11 <130> FILE REFERENCE: DV/4-33628A/GEP US-P
 13 <140> CURRENT APPLICATION NUMBER: 10/561,292
 14 <141> CURRENT FILING DATE: 2005-12-20
 16 <150> PRIOR APPLICATION NUMBER: 60/484,153
 17 <151> PRIOR FILING DATE: 2003-06-30
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/007047
 20 <151> PRIOR FILING DATE: 2004-06-29
 22 <160> NUMBER OF SEQ ID NOS: 8
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 456
 28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: PROPEP
33 <222> LOCATION: (1)...(456)
34 <223> OTHER INFORMATION: Precursor protein of CP22
36 <400> SEQUENCE: 1
37 Met Ile Leu Ser Leu Leu Phe Ser Leu Gly Gly Pro Leu Gly Trp Gly
38 1 5
                                    10
39 Leu Leu Gly Ala Trp Ala Gln Ala Ser Ser Thr Ser Leu Ser Asp Leu
40
             20
                                 25
41 Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr
42 35
                             40
43 Gly Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys
44 50
                         55
45 Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His
                     70
47 Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Lys Val Lys
                                    90
49 Val Met Tyr Arg Met Ala His Lys Pro Val Tyr Gln Val Lys Gln Lys
            100
                                105
51 Val Leu Thr Ser Leu Ala Trp Arg Cys Cys Pro Gly Tyr Thr Gly Pro
52 115
                             120
53 Asn Cys Glu His His Asp Ser Met Ala Ile Pro Glu Pro Ala Asp Pro
                         135
55 Gly Asp Ser His Gln Glu Pro Gln Asp Gly Pro Val Ser Phe Lys Pro
56 145 150
                                       155
```

57 Gly His Leu Ala Ala Val Ile Asn Glu Val Glu Val Gln Gln Glu Gln

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```
58
                                        170
 59 Gln Glu His Leu Leu Gly Asp Leu Gln Asn Asp Val His Arg Val Ala
                180
                                   185
 61 Asp Ser Leu Pro Gly Leu Trp Lys Ala Leu Pro Gly Asn Leu Thr Ala
 62 195
                                200
 63 Ala Ser Leu Ser Asn Asp Val Lys Asn Val Gly Arg Cys Cys Glu Ala
                            215
 65 Glu Ala Gly Ala Gly Ala Ala Ser Leu Asn Ala Ser Leu His Gly Leu
                        230
                                            235
 67 His Asn Ala Leu Phe Ala Thr Gln Arg Ser Leu Glu Gln His Gln Arg
                    245
                                       250
 69 Leu Phe His Ser Leu Phe Gly Asn Phe Gln Gly Leu Met Glu Ala Asn
                260
                                    265
 71 Val Ser Leu Asp Leu Gly Lys Leu Gln Thr Met Leu Ser Arg Lys Gly
                               280
 73 Lys Lys Gln Gln Lys Asp Leu Glu Ala Pro Arg Lys Arg Asp Lys Lys
                           295
 75 Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly
                       310
                                           315
 77 Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr
                   325
                                       330
 79 Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn
               340
                                   345
81 Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr
     355
                               360
83 Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu
    370
                           375
85 Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His
                      390
                                           395
87 Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr
                   405
                                       410
89 Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu
              420
                                  425
91 Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe
92 435
                               440
93 Gly Gly Phe Leu Met Phe Lys Thr
94 450
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 433
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <220> FEATURE:
103 <221> NAME/KEY: PEPTIDE
104 <222> LOCATION: (1) ... (433)
105 <223> OTHER INFORMATION: Polypeptide sequence of SEQ ID NO:1 after removal
106 of the signal peptide
108 <400> SEQUENCE: 2
109 Ala Ser Ser Thr Ser Leu Ser Asp Leu Gln Ser Ser Arg Thr Pro Gly
110 1
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111 Val Trp Lys Ala Glu Ala Glu Asp Thr Ser Lys Asp Pro Val Gly Arg 113 Asn Trp Cys Pro Tyr Pro Met Ser Lys Leu Val Thr Leu Leu Ala Leu 114 35 40 115 Cys Lys Thr Glu Lys Phe Leu Ile His Ser Gln Gln Pro Cys Pro Gln 117 Gly Ala Pro Asp Cys Gln Lys Val Lys Val Met Tyr Arg Met Ala His 70 119 Lys Pro Val Tyr Gln Val Lys Gln Lys Val Leu Thr Ser Leu Ala Trp 85 90 121 Arg Cys Cys Pro Gly Tyr Thr Gly Pro Asn Cys Glu His His Asp Ser 100 105 123 Met Ala Ile Pro Glu Pro Ala Asp Pro Gly Asp Ser His Gln Glu Pro 115 120 125 Gln Asp Gly Pro Val Ser Phe Lys Pro Gly His Leu Ala Ala Val Ile 135 127 Asn Glu Val Glu Gln Gln Gln Gln Gln His Leu Leu Gly Asp 150 155 129 Leu Gln Asn Asp Val His Arg Val Ala Asp Ser Leu Pro Gly Leu Trp 165 170 131 Lys Ala Leu Pro Gly Asn Leu Thr Ala Ala Ser Leu Ser Asn Asp Val 132 180 185 133 Lys Asn Val Gly Arg Cys Cys Glu Ala Glu Ala Gly Ala Gly Ala Ala 134 195 200 135 Ser Leu Asn Ala Ser Leu His Gly Leu His Asn Ala Leu Phe Ala Thr 136 210 215 220 137 Gln Arg Ser Leu Glu Gln His Gln Arg Leu Phe His Ser Leu Phe Gly 230 235 139 Asn Phe Gln Gly Leu Met Glu Ala Asn Val Ser Leu Asp Leu Gly Lys 245 250 141 Leu Gln Thr Met Leu Ser Arg Lys Gly Lys Lys Gln Gln Lys Asp Leu 260 265 143 Glu Ala Pro Arg Lys Arg Asp Lys Lys Glu Ala Glu Pro Leu Val Asp 280 145 Ile Arg Val Thr Gly Pro Val Pro Gly Ala Leu Gly Ala Ala Leu Trp 146 290 295 147 Glu Ala Gly Ser Pro Val Ala Phe Tyr Ala Ser Phe Ser Glu Gly Thr 310 315 149 Ala Ala Leu Gln Thr Val Lys Phe Asn Thr Thr Tyr Ile Asn Ile Gly 325 330 151 Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Glu Arg Gly 340 345 153 Val Tyr Leu Phe Ala Val Ser Val Glu Phe Gly Pro Gly Pro Gly Thr 154 355 360 155 Gly Gln Leu Val Phe Gly Gly His His Arg Thr Pro Val Cys Thr Thr 375 157 Gly Gln Gly Ser Gly Ser Thr Ala Thr Val Phe Ala Met Ala Glu Leu 390 395 159 Gln Lys Gly Glu Arg Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr

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```
160
                                          410
 161 Lys Arg Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys
 162
                 420
                                      425
 163 Thr
 167 <210> SEQ ID NO: 3
 168 <211> LENGTH: 152
 169 <212> TYPE: PRT
 170 <213> ORGANISM: Homo sapiens
 172 <220> FEATURE:
 173 <221> NAME/KEY: PEPTIDE
 174 <222> LOCATION: (1) ... (152)
 175 <223> OTHER INFORMATION: Cardiovascular disorder Plasma Polypeptide 22 (CPP
 176
          22)
 178 <400> SEQUENCE: 3
 179 Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly
                                         10
 181 Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr
 183 Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn
 184
             35
 185 Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr
187 Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu
                                             75
189 Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His
                     85
191 Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr
                100
                                     105
193 Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu
                                 120
                                                     125
195 Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe
        130
                             135
197 Gly Gly Phe Leu Met Phe Lys Thr
198 145
                        150
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 24
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <220> FEATURE:
207 <221> NAME/KEY: PEPTIDE
208 <222> LOCATION: (1) ... (24)
209 <223> OTHER INFORMATION: Tryptic peptides of CPP 22 found by MS-MS mass
         spectrometry in plasma samples of individuals with
211
          coronary artery disease
213 <400> SEQUENCE: 4
214 Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr Val
                                        10
216 Phe Ala Met Ala Glu Leu Gln Lys
```

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217

DATE: 01/11/2007 TIME: 09:48:35

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220 <210> SEO ID NO: 5
 221 <211> LENGTH: 12
 222 <212> TYPE: PRT
 223 <213> ORGANISM: Homo sapiens
 225 <220> FEATURE:
 226 <221> NAME/KEY: PEPTIDE
 227 <222> LOCATION: (1)...(12)
 228 <223> OTHER INFORMATION: Tryptic peptides of CPP 22 found by MS-MS mass
           spectrometry in plasma samples of individuals with
 229
           coronary artery disease
 232 <400> SEQUENCE: 5
 233 Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr Lys
 237 <210> SEQ ID NO: 6
 238 <211> LENGTH: 14
 239 <212> TYPE: PRT
 240 <213> ORGANISM: Homo sapiens
 242 <220> FEATURE:
 243 <221> NAME/KEY: PEPTIDE
 244 <222> LOCATION: (1)...(14)
245 <223> OTHER INFORMATION: Tryptic peptides of CPP 22 found by MS-MS mass
 246
          spectrometry in plasma samples of individuals with
 247
          coronary artery disease
 249 <400> SEQUENCE: 6
250 Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 1371
256 <212> TYPE: DNA
257 <213> ORGANISM: Homo sapiens
259 <220> FEATURE:
260 <221> NAME/KEY: variation
261 <222> LOCATION: (1)...(1371)
262 <223> OTHER INFORMATION: Splice variant of the Endoglyx-1 gene and
263
          comprises the cDNA coding sequence for SEQ ID NO:
264
          1
266 <400> SEQUENCE: 7
267 atgatectga gettgetgtt eageettggg ggeeceetgg getggggget getgggggea 60
268 tgggcccagg cttccagtac tagcctctct gatctgcaga gctccaggac acctggggtc 120
269 tggaaggcag aggctgagga caccggcaag gaccccgtag gacgtaactg gtgcccctac 180
270 ccaatgtcca agctggtcac cttactagct ctttgcaaaa cagagaaatt cctcatccac 240
271 tegeageage egtgteegea gggageteea gaetgeeaga aagteaaagt catgtacege 300
272 atggcccaca agccagtgta ccaggtcaag cagaaggtgc tgacctcttt ggcctggagg 360
273 tgctgccctg gctacacggg ccccaactgc gagcaccacg attccatggc aatccctgag 420
274 cctgcagatc ctggtgacag ccaccaggaa cctcaggatg gaccagtcag cttcaaacct 480
275 ggccaccttg ctgcagtgat caatgaggtt gaggtgcaac aggaacagca ggaacatctg 540
276 ctgggagatc tccagaatga tgtgcaccgg gtggcagaca gcctgccagg cctgtggaaa 600
277 gecetgeetg gtaaceteac agetgeaage etgageaacg aegteaagaa tgtegggegg 660
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278 tgctgcgagg ccgaggccgg ggccggggcc gcctccctca acgcctccct tcacggcctc 720

VERIFICATION SUMMARY

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